

#16



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,859

DATE: 02/05/2003

TIME: 08:13:12

Input Set : A:\KATO SEQUENCE LISTING.txt

Output Set: N:\CRF4\02052003\J088859.raw

3 <110> APPLICANT: KATO, Seishi
4 NAGATA, Naoki
5 FUJIMURA, Naoko
6 KOBAYASHI, Midori
7 ITO, Koichi
8 ISHIZUKA, Yoshiko
10 <120> TITLE OF INVENTION: A Method for Producing an Antibody by Gene Immunization
12 <130> FILE REFERENCE: 2002-0400A/LC/00653
14 <140> CURRENT APPLICATION NUMBER: 10/088,859
15 <141> CURRENT FILING DATE: 2002-05-29
17 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06371
18 <151> PRIOR FILING DATE: 2001-07-24
20 <150> PRIOR APPLICATION NUMBER: JP2000-222743
21 <151> PRIOR FILING DATE: 2000-07-24
23 <150> PRIOR APPLICATION NUMBER: JP2000-254407
24 <151> PRIOR FILING DATE: 2000-08-24
26 <160> NUMBER OF SEQ ID NOS: 13
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 697
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (151)..(600)
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42 aataaagtta caactttgaa gagagtttct gcaagacatg acacaaagct gctagcagaa 120
44 aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt 174
45 Met Met Thr Lys His Lys Lys Cys
46 1 5
48 ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata 222
49 Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
50 10 15 20
52 gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270
53 Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
54 25 30 35 40
56 ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318
57 Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
58 45 50 55
60 aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata 366
61 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
62 60 65 70

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64 att gac aac ata gaa gaa atg aat ttt ctt agg cgg tat aaa tgc agt 414
65 Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
66      75      80      85
68 tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa 462
69 Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
70      90      95      100
72 tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt 510
73 Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
74 105      110      115      120
76 gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt 558
77 Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
78      125      130      135
80 tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa 600
81 Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
82      140      145
84 gttaatgtct aagataatgg ggaaaataga aaataacatt attaagtgtgta aaaccagcaa 660
86 agtacttttt taattaaaca aagttcgagt tttgtac 697
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 149
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
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96 1 5 10 15
97 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
98 20 25 30
99 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
100 35 40 45
101 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
102 50 55 60
103 Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
104 65 70 75 80
105 Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
106 85 90 95
107 Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
108 100 105 110
109 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
110 115 120 125
111 Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
112 130 135 140
113 Arg Lys Arg Ile His
114 145
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120 <212> TYPE: DNA
121 <213> ORGANISM: Homo sapiens
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (30)..(503)

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130                                     1 5
132 gcg gtg gag gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc 101
133 Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile
134 10 15 20
136 agt gac gtg ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac 149
137 Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
138 25 30 35 40
140 aag gta tat gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att 197
141 Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
142 45 50 55
144 gag cga ctc cag gaa gct aag cac tcg gag tta tat atg cag gtg gat 245
145 Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp
146 60 65 70
148 ttg ggc tgt aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc 293
149 Leu Gly Cys Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg
150 75 80 85
152 atc tat gtg gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca 341
153 Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala
154 90 95 100
156 gaa gct ctc aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc 389
157 Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
158 105 110 115 120
160 agc aac agc ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac 437
161 Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
162 125 130 135
164 atg ttg cta gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca 485
165 Met Leu Leu Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro
166 140 145 150
168 gag aag cct cac cat tga cttcttcccc ccatactcag acattaaaga 533
169 Glu Lys Pro His His
170 155
172 gcctgaatgc ctttg 548
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 157
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 4
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182 1 5 10 15
183 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
184 20 25 30
185 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
186 35 40 45
187 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
188 50 55 60
189 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp

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190 65              70              75              80
191 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
192              85              90              95
193 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
194              100             105             110
195 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
196              115             120             125
197 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
198              130             135             140
199 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
200 145             150             155
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 30
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
211 <400> SEQUENCE: 5
212 cccgatatct catggcgacg cccctaagc 30
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 30
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
223 <400> SEQUENCE: 6
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227 <210> SEQ ID NO: 7
228 <211> LENGTH: 28
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
235 <400> SEQUENCE: 7
236 cccgaattca tggcgacgcc ccctaagc 28
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 32
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
246 <400> SEQUENCE: 8
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251 <211> LENGTH: 1643
252 <212> TYPE: DNA
253 <213> ORGANISM: Homo sapiens
255 <220> FEATURE:
256 <221> NAME/KEY: CDS

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257 <222> LOCATION: (25)..(915)

259 <400> SEQUENCE: 9

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262                               1           5
264 cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg      99
265 Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
266 10           15           20           25
268 caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt      147
269 Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
270           30           35           40
272 gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag      195
273 Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu
274           45           50           55
276 caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt      243
277 Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly
278           60           65           70
280 gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc      291
281 Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
282           75           80           85
284 cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag      339
285 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
286 90           95           100           105
288 gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg      387
289 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
290           110           115           120
292 cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg      435
293 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
294           125           130           135
296 aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc      483
297 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
298           140           145           150
300 tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag      531
301 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
302           155           160           165
304 aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct      579
305 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala
306 170           175           180           185
308 gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag      627
309 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln
310           190           195           200
312 gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc      675
313 Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser
314           205           210           215
316 aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt      723
317 Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe
318           220           225           230
320 gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga      771
321 Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly

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